



LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ANDERTON, STEPHEN MARK
VAN DER ZEE, RUURD
VAN EDEN, WILLEM

(ii) TITLE OF INVENTION: PEPTIDE FRAGMENTS OF MICROBIAL STRESS
PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE
TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: THE WEBB LAW FIRM

(B) STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE

(C) CITY: PITTSBURGH

(D) STATE: PENNSYLVANIA

(E) COUNTRY: UNITED STATES OF AMERICA

(F) ZIP: 15219-1818

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" FLOPPY DISK

(B) COMPUTER: DIGITAL VENTURIS GL 6200

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: MICROSOFT WORD 2.0c

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/716,169

(B) FILING DATE: 18-SEP-1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/NL95/00108

(B) FILING DATE: 21-MAR-1995

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met	Ala	Lys	Thr	Ile	Ala	Tyr	Asp	Glu	Glu	Ala	Arg	Arg	Gly	Leu
1				5					10					15
Glu	Arg	Gly	Leu	Asn	Ala	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu
			20						25					30
Gly	Pro	Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Lys	Trp	Gly	Ala
			35						40					45
Pro	Thr	Ile	Thr	Asn	Asp	Gly	Val	Ser	Ile	Ala	Lys	Glu	Ile	Glu
			50						55					60
Leu	Glu	Asp	Pro	Tyr	Glu	Lys	Ile	Gly	Ala	Glu	Leu	Val	Lys	Glu
			65						70					75
Val	Ala	Lys	Lys	Thr	Asp	Asp	Val	Ala	Gly	Asp	Gly	Thr	Thr	Thr
			80						85					90

Ala	Thr	Val	Leu	Ala	Gln	Ala	Leu	Val	Arg	Glu	Gly	Leu	Arg	Asn
				95					100					105
Val	Ala	Ala	Gly	Ala	Asn	Pro	Leu	Gly	Val	Lys	Arg	Gly	Ile	Glu
				110					115					120
Lys	Ala	Val	Glu	Lys	Val	Thr	Glu	Thr	Leu	Leu	Lys	Gly	Ala	Lys
				125					130					135
Glu	Val	Glu	Thr	Lys	Glu	Gln	Ile	Ala	Ala	Thr	Ala	Ala	Ile	Ser
				140					145					150
Ala	Gly	Asp	Gln	Ser	Ile	Gly	Asp	Leu	Ile	Ala	Glu	Ala	Met	Asp
				155					160					165
Lys	Val	Gly	Asn	Glu	Gly	Val	Ile	Thr	Val	Glu	Glu	Ser	Asn	Thr
				170					175					180
Phe	Gly	Leu	Gln	Leu	Glu	Leu	Thr	Glu	Gly	Met	Arg	Phe	Asp	Lys
				185					190					195
Gly	Tyr	Ile	Ser	Gly	Tyr	Phe	Val	Thr	Asp	Pro	Glu	Arg	Gln	Glu
				200					205					210
Ala	Val	Leu	Glu	Asp	Pro	Tyr	Ile	Leu	Leu	Val	Ser	Ser	Lys	Val
				215					220					225
Ser	Thr	Val	Lys	Asp	Leu	Leu	Pro	Leu	Leu	Glu	Lys	Val	Ile	Gly
				230					235					240
Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu
				245					250					255
Ala	Leu	Ser	Thr	Leu	Val	Val	Asn	Lys	Ile	Arg	Gly	Thr	Phe	Lys
				260					265					270
Ser	Val	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala
				275					280					285
Met	Leu	Gln	Asp	Met	Ala	Ile	Leu	Thr	Gly	Gly	Gln	Val	Ile	Ser
				290					295					300
Glu	Glu	Val	Gly	Leu	Thr	Leu	Glu	Asn	Ala	Asp	Leu	Ser	Leu	Leu
				305					310					315
Gly	Lys	Ala	Arg	Lys	Val	Val	Val	Thr	Lys	Asp	Glu	Thr	Thr	Ile
				320					325					330
Val	Glu	Gly	Ala	Gly	Asp	Thr	Asp	Ala	Ile	Ala	Gly	Arg	Val	Ala
				335					340					345

Gln Ile Arg Gln Glu Ile Glu Asn Ser Asp Ser Asp Tyr Asp Arg
 350 355 360
 Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ala Gly Gly Val Ala
 365 370 375
 Val Ile Lys Ala Gly Ala Ala Thr Glu Val Glu Leu Lys Glu Arg
 380 385 390
 Lys His Arg Ile Glu Asp Ala Val Arg Asn Ala Lys Ala Ala Val
 395 400 405
 Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr Leu Leu Gln Ala
 410 415 420
 Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp Glu Ala Thr
 425 430 435
 Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu Lys Gln
 440 445 450
 Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu Lys
 455 460 465
 Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly
 470 475 480
 Val Lys Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys
 485 490 495
 Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu
 500 505 510
 Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu
 515 520 525
 Lys Ala Ser Val Pro Gly Gly Gly Asp Met Gly Gly Met Asp Phe
 530 535 540

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
 1 5 10 15
 Val Phe Arg Ala Ala Leu Lys Asn Pro Asp Ile Glu Val Val Ala
 20 25 30

Val Asn Asp Leu Thr Asp Ala Asn Thr Leu Ala His Leu Leu Lys
 35 40 45
 Tyr Asp Ser Val His Gly Arg Leu Asp Ala Glu Val Ser Val Asn
 50 55 60
 Gly Asn Asn Leu Val Val Asn Gly Lys Glu Ile Ile Val Lys Ala
 65 70 75
 Glu Arg Asp Pro Glu Asn Leu Ala Trp Gly Glu Ile Gly Val Asp
 80 85 90
 Ile Val Val Glu Ser Thr Gly Arg Phe Thr Lys Arg Glu Asp Ala
 95 100 105
 Ala Lys His Leu Glu Ala Gly Ala Lys Lys Val Ile Ile Ser Ala
 110 115 120
 Pro Ala Lys Asn Glu Asp Ile Thr Ile Val Met Gly Val Asn Gln
 125 130 135
 Asp Lys Tyr Asp Pro Lys Ala His His Val Ile Ser Asn Ala Ser
 140 145 150
 Cys Thr Thr Asn Cys Leu Ala Pro Phe Ala Lys Val Leu His Glu
 155 160 165
 Gln Phe Gly Ile Val Arg Gly Met Met Thr Thr Val His Ser Tyr
 170 175 180
 Thr Asn Asp Gln Arg Ile Leu Asp Leu Pro His Lys Asp Leu Arg
 185 190 195
 Arg Ala Arg Ala Ala Ala Glu Ser Ile Ile Pro Thr Thr Thr Gly
 200 205 210
 Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys
 215 220 225
 Leu Asn Gly Met Ala Met Arg Val Pro Thr Pro Asn Val Ser Val
 230 235 240
 Val Asp Leu Val Ala Glu Leu Glu Lys Glu Val Thr Val Glu Glu
 245 250 255
 Val Asn Ala Ala Leu Lys Ala Ala Ala Glu Gly Glu Leu Lys Gly
 260 265 270
 Ile Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Arg Asp Tyr Asn
 275 280 285

Gly Ser Thr Val Ser Ser Thr Ile Asp Ala Leu Ser Thr Met Val
290 295 300

Ile Asp Gly Lys Met Val Lys Val Val Ser Trp Tyr Asp Asn Glu
305 310 315

Thr Gly Tyr Ser His Arg Val Val Asp Leu Ala Ala Tyr Ile Ala
320 325 330

Ser Lys Gly

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val
1 5 10 15

Thr Arg Ala Ala Phe Ser Cys Asp Lys Val Asp Ile Val Ala Ile
20 25 30

Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
35 40 45

Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu
50 55 60

Asn Gly Lys Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln
65 70 75

Glu Arg Asp Pro Val Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu
80 85 90

Tyr Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala
95 100 105

Gly Ala His Leu Lys Gly Gly Ala Lys Arg Val Ile Ile Ser Ala
110 115 120

Pro Ser Ala Asp Ala Pro Met Phe Val Met Gly Val Asn His Glu
125 130 135

Lys Tyr Asp Asn Ser Leu Lys Ile Val Ser Asn Ala Ser Cys Thr
140 145 150

Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp Asn Phe
155 160 165

Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala Ile Thr Ala 170
 175
 Thr Gln Lys Thr Val Asp Gly Pro Ser Gly Lys Leu Trp Arg Asp 185
 190
 Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Ala Ser Thr Gly Ala 200
 205
 Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly Lys Leu 215
 220
 Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asn Val Ser Val Val 230
 235
 Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile 245
 250
 Lys Lys Val Val Lys Gln Ala Ala Glu Gly Pro Leu Lys Gly Ile 260
 265
 Leu Gly Tyr Thr Glu Asp Gln Val Val Ser Cys Asp Phe Asn Ser 275
 280
 Asn Ser His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu 290
 295
 Asn Asp Asn Ile Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr 305
 310
 Gly Tyr Ser Asn Arg Val Val Asp Leu Met Ala Tyr Met Ala Ser 320
 325
 Lys Glu

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser 1 5 10 15

Arg Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val 20 25 30

Lys Phe Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp 35 40 45

Leu Leu Ala Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg
 50 55 60
 Thr Val Ile Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys
 65 70 75
 Asp Gly Val Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr
 80 85 90
 Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr
 95 100 105
 Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
 110 115 120
 Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala
 125 130 135
 Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala
 140 145 150
 Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro
 155 160 165
 Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys
 170 175 180
 Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg
 185 190 195
 Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu
 200 205 210
 Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser
 215 220 225
 Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
 230 235 240
 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln
 245 250 255
 Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro
 260 265 270
 Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr
 275 280 285
 Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val
 290 295 300

Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp 315
 305 310
 Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu 330
 320 325
 Thr Leu Asn Leu Glu Asp Val Gln Pro His Asp Leu Gly Lys Val 345
 335 340
 Gly Glu Val Ile Val Thr Lys Asp Asp Ala Met Leu Leu Lys Gly 360
 350 355
 Lys Gly Asp Lys Ala Gln Ile Glu Lys Arg Ile Gln Glu Ile Ile 375
 365 370
 Glu Gln Leu Asp Val Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu 390
 380 385
 Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys 405
 395 400
 Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu Lys Lys Asp Arg 420
 410 415
 Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly 435
 425 430
 Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala 450
 440 445
 Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly Ile 465
 455 460
 Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala 480
 470 475
 Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met 495
 485 490
 Gln Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe 510
 500 505
 Val Asn Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val 525
 515 520
 Arg Thr Ala Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr 540
 530 535
 Thr Ala Glu Val Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp 555
 545 550

Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly
560 565 570

Gly Met Phe

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 547

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ala	Lys	Asp	Val	Lys	Phe	Gly	Ala	Asp	Ala	Arg	Ala	Leu	Met	Leu	1	5	10	15
Gln	Gly	Val	Asp	Leu	Leu	Ala	Asp	Ala	Val	Ala	Val	Thr	Met	Gly	20	25	30	
Pro	Lys	Gly	Arg	Thr	Val	Ile	Ile	Glu	Gln	Ser	Trp	Gly	Ser	Pro	35	40	45	
Lys	Val	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	Asp	Leu	50	55	60	
Lys	Asp	Lys	Tyr	Lys	Asn	Ile	Gly	Ala	Lys	Leu	Val	Gln	Asp	Val	65	70	75	
Ala	Asn	Asn	Thr	Asn	Glu	Glu	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	80	85	90	
Thr	Val	Leu	Ala	Arg	Ser	Ile	Ala	Lys	Glu	Gly	Phe	Glu	Lys	Ile	95	100	105	
Ser	Lys	Gly	Ala	Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val	Met	Leu	110	115	120	
Ala	Val	Asp	Ala	Val	Ile	Ala	Glu	Leu	Lys	Lys	Gln	Ser	Lys	Pro	125	130	135	
Val	Thr	Thr	Pro	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	140	145	150	
Asn	Gly	Asp	Lys	Asp	Ile	Gly	Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	155	160	165	
Lys	Val	Gly	Arg	Lys	Gly	Val	Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	170	175	180	
Leu	Asn	Asp	Glu	Leu	Glu	Ile	Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	185	190	195	

Gly Tyr Ile Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys
 200 205 210
 Cys Glu Phe Gln Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile
 215 220 225
 Ser Ser Val Gln Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala
 230 235 240
 His Arg Lys Pro Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu
 245 250 255
 Ala Leu Ser Thr Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln
 260 265 270
 Val Val Ala Val Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn
 275 280 285
 Gln Leu Lys Asp Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly
 290 295 300
 Glu Glu Gly Leu Asn Leu Asn Leu Glu Asp Val Gln Ala His Asp
 305 310 315
 Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys Asp Asp Ala Met
 320 325 330
 Leu Leu Lys Gly Lys Gly Asp Lys Ala His Ile Glu Lys Arg Ile
 335 340 345
 Gln Glu Ile Thr Glu Gln Leu Asp Ile Thr Thr Ser Glu Tyr Glu
 350 355 360
 Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly Val
 365 370 375
 Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
 380 385 390
 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala
 395 400 405
 Val Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg
 410 415 420
 Cys Ile Pro Ala Leu Asp Ser Leu Lys Pro Ala Asn Glu Asp Gln
 425 430 435
 Lys Ile Gly Ile Glu Ile Ile Lys Arg Ala Leu Lys Ile Pro Ala
 440 445 450

Met Thr Ile Ala Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val 465
 455
 Glu Lys Ile Leu Gln Ser Ser Ser Glu Val Gly Tyr Asp Ala Met 480
 470
 Leu Gly Asp Phe Val Asn Met Val Glu Lys Gly Ile Ile Asp Pro 495
 485
 Thr Lys Val Val Arg Thr Ala Leu Leu Asp Ala Ala Gly Val Ala 510
 500
 Ser Leu Leu Thr Thr Ala Glu Ala Val Val Thr Glu Ile Pro Lys 525
 515
 Glu Glu Lys Asp Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly 540
 530
 Gly Met Gly Gly Gly Met Phe 545

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 555

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe Gly 15
 1 5 10
 Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala 30
 20 25
 Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile 45
 35 40
 Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val 60
 50 55
 Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile 75
 65 70
 Gly Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu 90
 80 85
 Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile 105
 95 100
 Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala Asn Pro Val 120
 110 115

Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala Val Ile Ala 135
 125 130
 Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro Glu Glu Ile 150
 140 145
 Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys Asp Ile Gly 165
 155 160
 Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg Lys Gly Val 180
 170 175
 Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu Leu Glu Ile 195
 185 190
 Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe 210
 200 205
 Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln Asp Ala Tyr 225
 215 220
 Val Leu Leu Ser Glu Lys Lys Phe Ser Ser Val Gln Ser Ile Val 240
 230 235
 Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val Ile 255
 245 250
 Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu 270
 260 265
 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro 285
 275 280
 Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile 300
 290 295
 Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Asn Leu Asn 315
 305 310
 Leu Glu Asp Val Gln Ala His Asp Leu Gly Lys Val Gly Glu Val 330
 320 325
 Ile Val Thr Lys Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp 345
 335 340
 Lys Ala His Ile Glu Lys Arg Ile Gln Glu Ile Thr Glu Gln Leu 360
 350 355
 Asp Ile Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu Asn Glu Arg 375
 365 370

Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys Val Gly Gly
 380 385 390
 Thr Ser Asp Val Glu Val Asn Glu Lys Lys Asp Arg Val Thr Asp
 395 400 405
 Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Leu
 410 415 420
 Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala Leu Asp Ser
 425 430 435
 Leu Lys Pro Ala Asn Glu Asp Gln Lys Ile Gly Ile Glu Ile Ile
 440 445 450
 Lys Arg Ala Leu Lys Ile Pro Ala Met Thr Ile Ala Lys Asn Ala
 455 460 465
 Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Leu Gln Ser Ser
 470 475 480
 Ser Glu Val Gly Tyr Asp Ala Met Leu Gly Asp Phe Val Asn Met
 485 490 495
 Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
 500 505 510
 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu
 515 520 525
 Ala Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met
 530 535 540
 Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
 545 550 555